

[At page 2, replace the second full paragraph as follows:]

--The invention features a nucleic acid molecule which includes a fragment of at least 300 (e.g., 325, 350, 375, 400, 425, 450, 500, 550, 600, 650, 700, 800, 900, 1000, 1200, 1400, 1600, or 1770) nucleotides of the nucleotide sequence shown in SEQ ID NO:1, or SEQ ID NO:3, or the nucleotide sequence of the cDNA ATCC PTA-1663, or a complement thereof.--

[At page 2, replace the third full paragraph as follows:]

--The invention also features a nucleic acid molecule which includes a nucleotide sequence encoding a protein having an amino acid sequence that is at least 65% (or 75%, 85%, 95%, or 98%) identical to the amino acid sequence of SEQ ID NO:2 or the amino acid sequence encoded by the cDNA of ATCC PTA-1663.--

[At page 2, replace the fourth full paragraph as follows:]

--Also within the invention is a nucleic acid molecule that encodes a fragment of a polypeptide having the amino acid sequence of SEQ ID NO:2, the fragment including at least 15 (25, 30, 50, 100, 150, 300, 400, or 450) contiguous amino acids of SEQ ID NO:2 or the polypeptide encoded by the cDNA of ATCC Accession Number PTA-1663.--

At page 3, replace the first paragraph starting at line 1 as follows:

--NMT protein which is encoded by a nucleic acid molecule having a nucleotide sequence that is at least about 65% (e.g., 75%, 85%, or 95%) identical to SEQ ID NO:1 or the cDNA of ATCC PTA-1663; and an isolated NMT protein which is encoded by a nucleic acid molecule having a nucleotide sequence which hybridizes under stringent hybridization conditions to a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:1 or the non-coding strand of the cDNA of ATCC PTA-1663.--

[At page 3, replace the first full paragraph starting at line 10 as follows:]

--Another embodiment of the invention features NMT nucleic acid molecules which specifically detect *Aspergillus* NMT nucleic acid molecules relative to nucleic acid molecules encoding other

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N-myristoyltransferases. For example, in one embodiment, an *Aspergillus* NMT nucleic acid molecule hybridizes under stringent conditions to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, or the cDNA of ATCC PTA-1663, or a complement thereof. In another embodiment, the *Aspergillus* NMT nucleic acid molecule is at least 300 (e.g., 400, 500, 700, 900, 1100, or 1300) nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising the nucleotide sequence shown in SEQ ID NO:1, SEQ ID NO:3, the cDNA of ATCC PTA-1663, or a complement thereof. In another embodiment, the invention provides an isolated nucleic acid molecule which is antisense to the coding strand of an *Aspergillus* NMT nucleic acid.--

At page 12, replace the second paragraph beginning at line 5 as follows:

--Figs. 1A and 1B are a listing of the nucleotide sequence (SEQ ID NO:1) and predicted amino acid sequence (SEQ ID NO:2) of *Aspergillus fumigatus* N-myristoyl transferase (NMT).--

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[At page 12, replace the third paragraph beginning at line 8 as follows:]

--Figs. 2A to 2C are a listing of the genomic (SEQ ID NO:3) and predicted amino acid sequences (SEQ ID NO:2) of *Aspergillus fumigatus* NMT.--

At page 14, replace the first full paragraph starting at line 9 as follows:

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--A nucleic acid sequence that is substantially identical to an essential nucleotide sequence is at least 80% identical to the nucleotide sequence of NMT as represented by the SEQ ID NOs:1 and 3, as depicted in Figs. 1A to 1B and 2A to 2C. For purposes of comparison of nucleic acids, the length of the reference nucleic acid sequence will generally be at least 40 nucleotides, e.g., at least 60 nucleotides or more nucleotides.--

--Preferred NMT polypeptides include a sequence substantially identical to all or a portion of a naturally occurring *Aspergillus* NMT polypeptide, e.g., including all or a portion of the sequences shown in Figs. 2A to 2C. Polypeptides "substantially identical" to the NMT polypeptide sequences described herein have an amino acid sequence that is at least 65% identical to the amino acid sequence of the NMT polypeptide represented by the SEQ ID NO:2 (measured as described herein). The new polypeptides can also have a greater percentage identity, e.g., 85%, 90%, 95%, or even higher. For purposes of comparison, the length of the--

Cancel claims 1 to 41.